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DATE: 09/26/2002

PATENT APPLICATION: US/10/024,399

TIME: 16:47:12

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3 <110> APPLICANT: Padigar, Muralidhara
4 Kekuda, Ramesh
5 Colman, Steven D.
6 Spytek, Kimberly A.
7 Ballinger, Robert A.
8 Vernet, Corine A.M.
9 Li, Li
10 Shenoy, Suresh G.
11 Casman, Stacie J.
13 <120> TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
15 <130> FILE REFERENCE: 21402-224AE
17 <140> CURRENT APPLICATION NUMBER: 10/024,399
18 <141> CURRENT FILING DATE: 2001-12-18
20 <150> PRIOR APPLICATION NUMBER: 60/256,635
21 <151> PRIOR FILING DATE: 2000-12-18
23 <150> PRIOR APPLICATION NUMBER: 60/259,743
24 <151> PRIOR FILING DATE: 2001-01-04
26 <150> PRIOR APPLICATION NUMBER: 60/299,327
27 <151> PRIOR FILING DATE: 2001-06-19
29 <150> PRIOR APPLICATION NUMBER: 60/261,498
30 <151> PRIOR FILING DATE: 2001-01-12
32 <150> PRIOR APPLICATION NUMBER: 60/263,689
33 <151> PRIOR FILING DATE: 2001-01-24
35 <150> PRIOR APPLICATION NUMBER: 60/267,464
36 <151> PRIOR FILING DATE: 2001-02-08
38 <150> PRIOR APPLICATION NUMBER: 60/271,021
39 <151> PRIOR FILING DATE: 2001-02-22
41 <150> PRIOR APPLICATION NUMBER: 60/275,946
42 <151> PRIOR FILING DATE: 2001-03-14
44 <150> PRIOR APPLICATION NUMBER: 60/278,150
45 <151> PRIOR FILING DATE: 2001-03-23
47 <150> PRIOR APPLICATION NUMBER: 60/285,718
48 <151> PRIOR FILING DATE: 2001-04-23
50 <150> PRIOR APPLICATION NUMBER: 60/312,902
51 <151> PRIOR FILING DATE: 2001-08-16
53 <150> PRIOR APPLICATION NUMBER: 60/257,876
54 <151> PRIOR FILING DATE: 2000-12-21
56 <150> PRIOR APPLICATION NUMBER: 60/260,718
57 <151> PRIOR FILING DATE: 2001-01-10
59 <150> PRIOR APPLICATION NUMBER: 60/284,591
60 <151> PRIOR FILING DATE: 2001-04-18
62 <160> NUMBER OF SEQ ID NOS: 40
64 <170> SOFTWARE: PatentIn Ver. 2.1

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69 <213> ORGANISM: Homo sapiens
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73 ccaccagccg ggactgcgga tccccctctt cttcctgttt ctgggtttct acacggtcac 120
74 cgtggtgggg aacctgggct tgataaccct gattgggctg aactctcacc tgcacactcc 180
75 catgtacttc ttccctttta acctctcttt aatagatttc tgtttctcca ctaccatcac 240
76 tcccaaaatg ctgatgagtt ttgtctcaag gaagaacatc atttccttca cagggtgtat 300
77 gactcagctc ttcttcttct gcttctttgt cgtctctgag tccttcatcc tgtcagcgat 360
78 ggcgtatgac cgctacgtgg ccactctgtaa cccactgttg tacacagtca ccatgtcttg 420
79 ccaggtgtgt ttgtcctttt tgttgggtgc ctatgggatg gggtttgctg gggccatggc 480
80 ccacacagga agcataatga acctgacctt ctgtgctgac aaccttgtca atcatttcat 540
81 gtgtgacatc cttcctctcc ttgagctctc ctgcaacagc tcttacatga atgagctggt 600
82 ggtctttatt gtggtggctg ttgacgttgg aatgccatt gtcactgtct ttatttctta 660
83 tgccctcatc ctctccagca ttctacacaa cagtcttaca gaaggcaggc ccaaagcctt 720
84 tagtacttgc agttcccaca taattgtagt ttctcttttc tttggttctg gtgctttcat 780
85 gtatctcaaa cccctttcca tctgcccct cgagcaaggg aaagtgtcct ccctgttcta 840
86 taccataata gtccccgtgt taaaccatt aatctatagc ttgaggaaca aggatgtcaa 900
87 agttgccctg aggagaactt tgggcagaaa aatcttttct taagaaagca ggatggctaa 960
88 agggcacttg ggggaag                                     976

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100 Leu Thr His Gln Pro Gly Leu Arg Ile Pro Leu Phe Phe Leu Phe Leu
101           20           25           30
103 Gly Phe Tyr Thr Val Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu
104           35           40           45
106 Ile Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe
107           50           55           60
109 Asn Leu Ser Leu Ile Asp Phe Cys Phe Ser Thr Thr Ile Thr Pro Lys
110        65           70           75           80
112 Met Leu Met Ser Phe Val Ser Arg Lys Asn Ile Ile Ser Phe Thr Gly
113           85           90           95
115 Cys Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Val Ser Glu Ser
116           100          105          110
118 Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
119           115          120          125
121 Pro Leu Leu Tyr Thr Val Thr Met Ser Cys Gln Val Cys Leu Leu Leu
122           130          135          140
124 Leu Leu Gly Ala Tyr Gly Met Gly Phe Ala Gly Ala Met Ala His Thr
125        145          150          155          160
127 Gly Ser Ile Met Asn Leu Thr Phe Cys Ala Asp Asn Leu Val Asn His
128           165          170          175

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130 Phe Met Cys Asp Ile Leu Pro Leu Leu Glu Leu Ser Cys Asn Ser Ser
131      180      185      190
133 Tyr Met Asn Glu Leu Val Val Phe Ile Val Val Ala Val Asp Val Gly
134      195      200      205
136 Met Pro Ile Val Thr Val Phe Ile Ser Tyr Ala Leu Ile Leu Ser Ser
137      210      215      220
139 Ile Leu His Asn Ser Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr
140 225      230      235      240
142 Cys Ser Ser His Ile Ile Val Val Ser Leu Phe Phe Gly Ser Gly Ala
143      245      250      255
145 Phe Met Tyr Leu Lys Pro Leu Ser Ile Leu Pro Leu Glu Gln Gly Lys
146      260      265      270
148 Val Ser Ser Leu Phe Tyr Thr Ile Ile Val Pro Val Leu Asn Pro Leu
149      275      280      285
151 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Arg Thr
152      290      295      300
154 Leu Gly Arg Lys Ile Phe Ser
155 305      310
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159 <211> LENGTH: 963
160 <212> TYPE: DNA
161 <213> ORGANISM: Homo sapiens
163 <400> SEQUENCE: 3
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166 gcaggaaatc ttggcatgat tgccctcatc caggccaacc cccggctcca cacgcccattg 180
167 tactttttcc tgagcaactt atcctttgtg gatctgtgct tctcttccaa tgtgactcca 240
168 aggatgctgg agattttcct ttcagagaag aaaagcattt cctatcctgc ccgtcttgtg 300
169 cagtgttacc tttttatcac cttggtccac gttgagctct acatcctggc tgtgatggcc 360
170 tttgaccggt acatggccat ctgcaaccct ctgctttatg gcagcagaat gtccaagagc 420
171 gtgtgctctt tcctcatcac agtgctttat gtgtatggag cactcactgg cctgatggag 480
172 actatgtgga cctacaacct agccttctgt ggccccagtg aaattaatca cttctactgt 540
173 gtggaccac cactgattaa gctggcttgt tctgacacct acaacaagga ggtgtcaatg 600
174 tttgttgtgg ctggtttcaa cttcacttat cctctcctta tcctctcat ttcctatctc 660
175 tacatatttc ctgccacct aaggatctgc tctacagaag gcaggcacia agctttttct 720
176 acctgtggct cccatctgac agccgttact attttctatt cagctctttt cttcatgtat 780
177 ctgagacgtc catcagaaga gtccatggag caggggaaaa tggtagctgt attttatacc 840
178 actgtaatcc ccatgttgaa tcccatgatc tacagtctga ggaacaaaga tgtgaaagag 900
179 gcattatgca aagaactgtt caaaagaaaa ttgttttcta aataaacatt actactgatt 960
180 ttt
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184 <211> LENGTH: 312
185 <212> TYPE: PRT
186 <213> ORGANISM: Homo sapiens
188 <400> SEQUENCE: 4
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192 Ala Asn His Trp Glu Leu Gln Ile Phe Leu Phe Thr Leu Phe Leu Thr
193      20      25      30

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195 Ile Tyr Met Val Thr Val Ala Gly Asn Leu Gly Met Ile Ala Leu Ile
196           35                40                45
198 Gln Ala Asn Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
199           50                55                60
201 Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Arg Met
202    65                70                75                80
204 Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Arg
205                85                90                95
207 Leu Val Gln Cys Tyr Leu Phe Ile Thr Leu Val His Val Glu Leu Tyr
208                100               105               110
210 Ile Leu Ala Val Met Ala Phe Asp Arg Tyr Met Ala Ile Cys Asn Pro
211                115               120               125
213 Leu Leu Tyr Gly Ser Arg Met Ser Lys Ser Val Cys Ser Phe Leu Ile
214                130               135               140
216 Thr Val Leu Tyr Val Tyr Gly Ala Leu Thr Gly Leu Met Glu Thr Met
217   145                150                155                160
219 Trp Thr Tyr Asn Leu Ala Phe Cys Gly Pro Ser Glu Ile Asn His Phe
220                165                170                175
222 Tyr Cys Val Asp Pro Pro Leu Ile Lys Leu Ala Cys Ser Asp Thr Tyr
223                180                185                190
225 Asn Lys Glu Val Ser Met Phe Val Val Ala Gly Phe Asn Phe Thr Tyr
226                195                200                205
228 Pro Leu Leu Ile Ile Leu Ile Ser Tyr Leu Tyr Ile Phe Pro Ala Thr
229                210                215                220
231 Leu Arg Ile Cys Ser Thr Glu Gly Arg His Lys Ala Phe Ser Thr Cys
232   225                230                235                240
234 Gly Ser His Leu Thr Ala Val Thr Ile Phe Tyr Ser Ala Leu Phe Phe
235                245                250                255
237 Met Tyr Leu Arg Arg Pro Ser Glu Glu Ser Met Glu Gln Gly Lys Met
238                260                265                270
240 Val Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile
241                275                280                285
243 Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Cys Lys Glu Leu
244                290                295                300
246 Phe Lys Arg Lys Leu Phe Ser Lys
247   305                310
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251 <211> LENGTH: 964
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258 ccttattatt atcctgattc ttgtggatta caggctccac tcacccatgt atttcttctt 180
259 cagcaatctc tcttttcagt aaacattaac cataacctgt gctgttccta agatgctgga 240
260 gggcttcccg tcggaagga agagcatcac aagtggcgaa tgctctgcac agtcctattt 300
261 ctattttctt tccggatgca ctgagtttat tctttttgct gtcatgtcct atgaccgcta 360
262 tgtggccatt tgcagtcctc ttcagtacct tgcaattatg accagctcac tctgtgcca 420
263 cctcgtcatc ctctcctggg tgggtggctt tctcctcatg ctcccatcca ccatcctcaa 480

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264 ggcaggactg ccacactgtg gtcccaacgt gattgagcac tttttctgtg acagcgcccc 540
265 tctcctccac ctggcctgtg ctgacattcg tgctattgag ctgttggaact ttctcagctc 600
266 actggtcctg atcctcagct ccctctcaact cacagtggtc tcctatgttt acatcatctc 660
267 caccattctg aagataccct caggccaagg tcaacgcaaa gcctttgcca cctgtgcctc 720
268 tcacttcacg gtggctctccg tgggctatgg gatctccatc ttgtctatg ttcacccctc 780
269 acagaagagc agcctgcacc tcaacaagat cctctttatc ctctccagca tcatcacacc 840
270 cctcctgaat cccttcgtct tcagtctgtg gaatgaacct atgaaagatg cactgaagga 900
271 cgccctggcc ggaggacaga gcttgctcaa aggggtaagg tccacatgag gattctctga 960
272 gaat 964
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276 <211> LENGTH: 315
277 <212> TYPE: PRT
278 <213> ORGANISM: Homo sapiens
280 <400> SEQUENCE: 6
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282 1 5 10 15
284 Ile Pro Thr Thr Arg Ala Leu Gly Gly Leu Leu Phe Leu Ser Ala Tyr
285 20 25 30
287 Leu Val Thr Val Leu Gly Asn Thr Leu Ile Ile Ile Leu Ile Leu Val
288 35 40 45
290 Asp Tyr Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser
291 50 55 60
293 Phe Ser Glu Thr Leu Thr Ile Thr Cys Ala Val Pro Lys Met Leu Glu
294 65 70 75 80
296 Gly Phe Pro Ser Glu Arg Lys Ser Ile Thr Ser Gly Glu Cys Ser Ala
297 85 90 95
299 Gln Ser Tyr Phe Tyr Phe Leu Ser Gly Cys Thr Glu Phe Ile Pro Phe
300 100 105 110
302 Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu Gln
303 115 120 125
305 Tyr Pro Ala Ile Met Thr Ser Ser Leu Cys Ala His Leu Val Ile Leu
306 130 135 140
308 Ser Trp Val Gly Gly Phe Leu Leu Met Leu Pro Ser Thr Ile Leu Lys
309 145 150 155 160
311 Ala Gly Leu Pro His Cys Gly Pro Asn Val Ile Glu His Phe Phe Cys
312 165 170 175
314 Asp Ser Ala Pro Leu Leu His Leu Ala Cys Ala Asp Ile Arg Ala Ile
315 180 185 190
317 Glu Leu Leu Asp Phe Leu Ser Ser Leu Val Leu Ile Leu Ser Ser Leu
318 195 200 205
320 Ser Leu Thr Val Val Ser Tyr Val Tyr Ile Ile Ser Thr Ile Leu Lys
321 210 215 220
323 Ile Pro Ser Gly Gln Gly Gln Arg Lys Ala Phe Ala Thr Cys Ala Ser
324 225 230 235 240
326 His Phe Thr Val Val Ser Val Gly Tyr Gly Ile Ser Ile Phe Val Tyr
327 245 250 255
329 Val His Pro Ser Gln Lys Ser Ser Leu His Leu Asn Lys Ile Leu Phe
330 260 265 270
332 Ile Leu Ser Ser Ile Ile Thr Pro Leu Leu Asn Pro Phe Val Phe Ser

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